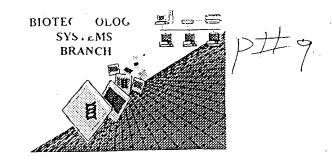# RAW SEQUENCE LISTING
ERROR REPORT

The Biotechnology Systems Branch of the Scientific and Technical Information Center (STIC) detected errors when processing the following computer readable form:

Application Serial Number: _09/654,281_

Source: _1642_

Date Processed by STIC: _5-14-01_

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MAY 3 1 2001

TECH CENTER 1600.2900

THE ATTACHED PRINTOUT EXPLAINS DETECTED ERRORS.
PLEASE FORWARD THIS INFORMATION TO THE APPLICANT BY EITHER:
1) INCLUDING A COPY OF THIS PRINTOUT IN YOUR NEXT COMMUNICATION TO THE APPLICANT, WITH A NOTICE TO COMPLY or,
2) TELEPHONING APPLICANT AND FAXING A COPY OF THIS PRINTOUT, WITH A NOTICE TO COMPLY
FOR CRF SUBMISSION QUESTIONS, PLEASE CONTACT MARK SPENCER, 703-308-4212.

FOR SEQUENCE RULES INTERPRETATION, PLEASE CONTACT ROBERT WAX, 703-308-4216.
PATENTIN 2.1 e-mail help: patin21help@uspto.gov or phone 703-306-4119 (R. Wax)
PATENTIN 3.0 e-mail help: patin3help@uspto.gov or phone 703-306-4119 (R. Wax)

TO REDUCE ERRORED SEQUENCE LISTINGS, PLEASE USE THE **CHECKER VERSION 3.0 PROGRAM**, ACCESSIBLE THROUGH THE U.S. PATENT AND TRADEMARK OFFICE WEBSITE. SEE BELOW:

Checker Version 3.0

The Checker Version 3.0 application is a state-of the-art Windows based software program employing a logical and intuitive user-interface to check whether a sequence listing is in compliance with format and content rules. Checker Version 3.0 works for sequence listings generated for the original version of 37 CFR §§1.821 – 1.825 effective October 1, 1990 (old rules) and the revised version (new rules) effective July 1, 1998 as well as World Intellectual Property Organization (WIPO) Standard ST.25.
Checker Version 3.0 replaces the previous DOS-based version of Checker, and is Y2K-compliant. Checker allows public users to check sequence listings in Computer Readable form (CRF) before submitting them to the United States Patent and Trademark Office (USPTO).
Use of Checker prior to filing the sequence listing is expected to result in fewer errored sequence listings, thus saving time and money.

Checker Version 3.0 can be down loaded from the USPTO website at the following address:
http://www.uspto.gov/web/offices/pac/checker

P- S _uence Listing Error S·ւ..m y

<u>ERROR DETECTED</u> <u>SUGGESTED CORRECTION</u>   SERIAL NUMBER: _09/654,281_

ATTN: NEW·RULES CASES: PLEASE DISREGARD ENGLISH "ALPHA" HEADERS, WHICH WERE INSERTED BY PTO SOFTWARE.

1 _____ Wrapped Nucleics   The number/text at the end of each line "wrapped" down to the next line.
This may occur if your file was retrieved in a word processor after creating it.
Please adjust your right margin to .3, as this will prevent "wrapping".

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MAY 3 1 2001

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2 _____ Wrapped Aminos   The amino acid number/text at the end of each line "wrapped " down to the next line.
This may occur if your file was retrieved in a word processor after creating it.
Please adjust your right margin to .3, as this will prevent "wrapping".

3 _____ Incorrect Line Length   The rules require that a line not exceed 72 characters in length. This includes spaces.

4 _____ Misaligned Amino Acid   The numbering under each 5th amino acid is misaligned. This may be caused by the use of tabs
Numbering   between the numbering. It is recommended to delete any tabs and use spacing between the numbers.

5 _____ Non-ASCII   This file was not saved in ASCII (DOS) text, as required by the Sequence Rules.
Please ensure your subsequent submission is saved in ASCII text so that it can be processed.

1, possibly more

6 ✓ Variable Length   Sequence(s) _1_ contain n's or Xaa's which represented more than one residue.
As per the rules, each n or Xaa can only represent a single residue.
Please present the maximum number of each residue having variable length and
indicate in the (x) feature section that some may be missing.
<221>

7 _____ PatentIn ver. 2.0 "bug"   A "bug" in PatentIn version 2.0 has caused the <220>-<223> section to be missing from amino acid
sequence(s) _____. Normally, PatentIn would automatically generate this section from the
previously coded nucleic acid sequence. Please manually copy the relevant <220>-<223> section
to the subsequent amino acid sequence. **This applies primarily to the mandatory <220>-<223>
sections for Artificial or Unknown sequences.**

8 _____ Skipped Sequences   Sequence(s) ____ missing. If intentional, please use the following format for each skipped sequence:
(OLD RULES)   (2) INFORMATION FOR SEQ ID NO:X:
(i) SEQUENCE CHARACTERISTICS:(Do not insert any headings under "SEQUENCE CHARACTERISTICS")
(xi) SEQUENCE DESCRIPTION:SEQ ID NO:X:
This sequence is intentionally skipped

Please also adjust the "(iii) NUMBER OF SEQUENCES:" response to include the skipped sequence(s).

9 _____ Skipped Sequences   Sequence(s) ____ missing. If intentional, please use the following format for each skipped sequence.
(NEW RULES)   <210> sequence id number
<400> sequence id number
000

10 _____ Use of n's or Xaa's   Use of n's and/or Xaa's have been detected in the Sequence Listing.
(NEW RULES)   Use of <220> to <223> is MANDATORY if n's or Xaa's are present.
In <220> to <223> section, please explain location of n or Xaa, and which residue n or Xaa represents.

11 ✓ Use of "Artificial"   Use of "Artificial" only as "<213> Organism" response is incomplete, per 1.823(b) of New Sequence Rules.
(NEW RULES)   Valid response is Artificial Sequence.

12 _____ Use of <220>Feature   Sequence(s) ____ are missing the <220>Feature and associated headings.
(NEW RULES)   Use of <220> to <223> is MANDATORY if <213>ORGANISM is "Artificial Sequence" or "Unknown"
Please explain source of genetic material in <220> to <223> section.
(See "Federal Register," 6/01/98, Vol. 63, No. 104, pp. 29631-32)   (Sec. 1.823 of new Rules)

13 _____ PatentIn ver. 2.0 "bug"   Please do not use "Copy to Disk" function of PatentIn version 2.0. This causes a corrupted
file, resulting in missing mandatory numeric identifiers and responses (as indicated on raw sequence listing).
Instead, please use "File Manager" or any other means to copy file to floppy disk.

AMC - Biotechnology Systems Branch - 4/06/2001

_09/654,281_

1642

RAW SEQUENCE LISTING   DATE: 05/14/2001
PATENT APPLICATION: US/09/654,281   TIME: 12:18:24

Does Not Comply
Corrected Diskette Needed
pp 1-2, 5

Input Set : A:\ES.txt
Output Set: N:\CRF3\05142001\I654281.raw

```
 3  <110> APPLICANT: Sedivy, John
 4        Kolch, Walter
 5        Yeung, Kam Chi
 7  <120> TITLE OF INVENTION: Kinase Inhibitors and Methods of Use in Screening Assays and Modulation
 8        of Cell Proliferation and Growth
10  <130> FILE REFERENCE: 3564/1010
12  <140> CURRENT APPLICATION NUMBER: 09/654,281
13  <141> CURRENT FILING DATE: 2000-09-01
15  <150> PRIOR APPLICATION NUMBER: 60/151,992
16  <151> PRIOR FILING DATE: 1999-09-01
18  <160> NUMBER OF SEQ ID NOS: 11
20  <170> SOFTWARE: PatentIn version 3.0
22  <210> SEQ ID NO: 1
23  <211> LENGTH: 42
24  <212> TYPE: PRT
25  <213> ORGANISM: Artificial
27  <220> FEATURE:
28  <223> OTHER INFORMATION: consensus sequence
30  <220> FEATURE:
31  <221> NAME/KEY: UNSURE
32  <222> LOCATION: (3)..(5)
33  <223> OTHER INFORMATION: Xaa = any amino acid
36  <220> FEATURE:
37  <221> NAME/KEY: UNSURE
38  <222> LOCATION: (9)..(9)
39  <223> OTHER INFORMATION: a hydrophobic amino acid residue
42  <220> FEATURE:
43  <221> NAME/KEY: UNSURE
44  <222> LOCATION: (11)..(13)
45  <223> OTHER INFORMATION: Xaa = any amino acid
48  <220> FEATURE:
49  <221> NAME/KEY: UNSURE
50  <222> LOCATION: (14)..(14)
51  <223> OTHER INFORMATION: a negatively charged amino acid residue
54  <220> FEATURE:
55  <221> NAME/KEY: UNSURE
56  <222> LOCATION: (15)..(18)
57  <223> OTHER INFORMATION: Xaa = any amino acid residue
60  <220> FEATURE:
61  <221> NAME/KEY: UNSURE
62  <222> LOCATION: (20)..(21)
63  <223> OTHER INFORMATION: Xaa = any amino acid residue
66  <220> FEATURE:
67  <221> NAME/KEY: UNSURE
68  <222> LOCATION: (23)..(23)
69  <223> OTHER INFORMATION: Xaa = 50 of any amino acid residue, 0 to 40 residues may be missi
70        n
```

C--> (handwritten annotations:)

Incomplete <213> response as per section 1.823b of new sequence rules. See #11 on the Error Summary Sheet.

Note: This error is also indicated in sequence #'s 10 and 11. Please review and correct.

5/14/01

```
RAW SEQUENCE LISTING                    DATE: 05/14/2001
PATENT APPLICATION: US/09/654,281       TIME: 12:18:24

Input Set : A:\ES.txt
Output Set: N:\CRF3\05142001\I654281.raw
```

```
 73 <220> FEATURE:
 74 <221> NAME/KEY: UNSURE
 75 <222> LOCATION: (25)..(28)
 76 <223> OTHER INFORMATION: Xaa = any amino acid residue
 79 <220> FEATURE:
 80 <221> NAME/KEY: UNSURE
 81 <222> LOCATION: (30)..(30)
 82 <223> OTHER INFORMATION: Xaa = 4 of any amino acid residue, 0 to 2 residues may be missing
 85 <220> FEATURE:
 86 <221> NAME/KEY: UNSURE
 87 <222> LOCATION: (32)..(32)
 88 <223> OTHER INFORMATION: Xaa = any amino acid residue
 91 <220> FEATURE:
 92 <221> NAME/KEY: UNSURE
 93 <222> LOCATION: (35)..(35)
 94 <223> OTHER INFORMATION: Xaa = an aromatic amino acid residue
 97 <220> FEATURE:
 98 <221> NAME/KEY: UNSURE
 99 <222> LOCATION: (37)..(37)
100 <223> OTHER INFORMATION: Xaa = any amino acid residue
103 <220> FEATURE:
104 <221> NAME/KEY: UNSURE
105 <222> LOCATION: (38)..(38)
106 <223> OTHER INFORMATION: a hydrophobic amino acid residue
109 <220> FEATURE:
110 <221> NAME/KEY: UNSURE
111 <222> LOCATION: (39)..(41)
112 <223> OTHER INFORMATION: Xaa = any amino acid residue
115 <400> SEQUENCE: 1
```

```
W--> 117 Thr Leu Xaa Xaa Xaa Asp Pro Asp Glx Pro Xaa Xaa Xaa Asx Xaa Xaa
     118 1               5                   10                  15
W--> 120 Xaa Xaa Glu Xaa Xaa His Xaa Tyr Xaa Xaa Xaa Xaa Pro Xaa Gly Xaa
     121             20                  25                  30
W--> 123 His Arg Xaa Val Xaa Glx Xaa Xaa Xaa Gln
     124         35                  40
```

```
126 <210> SEQ ID NO: 2
127 <211> LENGTH: 187
128 <212> TYPE: PRT
129 <213> ORGANISM: Homo sapiens
131 <400> SEQUENCE: 2
133 Met Pro Val Asp Leu Ser Lys Trp Ser Gly Pro Leu Ser Leu Gln Glu
134 1               5                   10                  15
136 Val Asp Glu Gln Pro Gln His Pro Leu His Val Thr Tyr Ala Gly Ala
137             20                  25                  30
139 Ala Val Asp Glu Leu Gly Lys Val Leu Thr Pro Thr Gln Val Lys Asn
140         35                  40                  45
142 Arg Pro Thr Ser Ile Ser Trp Asp Gly Leu Asp Ser Gly Lys Leu Tyr
143     50                  55                  60
145 Thr Leu Val Leu Thr Asp Pro Asp Ala Pro Ser Arg Lys Asp Pro Lys
```

"Xaa's" at positions 23 + 30 have variable length error. Each Xaa may only represent one residue. See Error # 6 on the Error Summary sheet.

RAW SEQUENCE LISTING   DATE: 05/14/2001
PATENT APPLICATION: US/09/654,281 TIME: 12:18:24

Input Set : A:\ES.txt
Output Set: N:\CRF3\05142001\I654281.raw

```
146 65                    70                75                80
148 Tyr Arg Glu Trp His His Phe Leu Val Val Asn Met Lys Gly Asn Asp
149                85                  90                95
151 Ile Ser Ser Gly Thr Val Leu Ser Asp Tyr Val Gly Ser Gly Pro Pro
152            100                105                110
154 Lys Gly Thr Gly Leu His Arg Tyr Val Trp Leu Val Tyr Glu Gln Asp
155         115                120                125
157 Arg Pro Leu Lys Cys Asp Glu Pro Ile Leu Ser Asn Arg Ser Gly Lys
158      130                135                140
160 His Arg Gly Lys Phe Lys Val Ala Ser Phe Arg Lys Lys Tyr Glu Leu
161 145              150                155                160
163 Arg Ala Pro Val Ala Gly Thr Cys Tyr Gln Ala Glu Trp Lys Lys Tyr
164            165                170                175
166 Val Pro Lys Leu Tyr Glu Gln Leu Ser Gly Lys
167            180                185
169 <210> SEQ ID NO: 3
170 <211> LENGTH: 187
171 <212> TYPE: PRT
172 <213> ORGANISM: Mus musculus
174 <220> FEATURE:
175 <221> NAME/KEY: UNSURE
176 <222> LOCATION: (150)..(150)
177 <223> OTHER INFORMATION: Xaa = any amino acid residue
180 <400> SEQUENCE: 3
182 Met Ala Ala Asp Ile Ser Gln Trp Ala Gly Pro Leu Cys Leu Gln Glu
183 1              5                  10                15
185 Val Asp Glu Pro Pro Gln His Ala Leu Arg Val Asp Tyr Ala Gly Val
186            20                25                30
188 Thr Val Asp Glu Leu Gly Lys Val Leu Thr Pro Thr Gln Val Met Asn
189         35                40                45
191 Arg Pro Ser Ser Ile Ser Trp Asp Gly Leu Asp Pro Gly Lys Leu Tyr
192    50                55                60
194 Thr Leu Val Leu Thr Asp Pro Asp Ala Pro Ser Arg Lys Asp Pro Lys
195 65                70                75                80
197 Phe Arg Glu Trp His His Phe Leu Val Val Asn Met Lys Gly Asn Asp
198                85                90                95
200 Ile Ser Ser Gly Thr Val Leu Ser Asp Tyr Val Gly Ser Gly Pro Pro
201            100                105                110
203 Ser Gly Thr Ser Ile His Arg Tyr Val Trp Leu Val Tyr Glu Gln Glu
204         115                120                125
206 Gln Pro Leu Ser Cys Asp Glu Pro Ile Leu Ser Asn Lys Ser Gly Asp
207      130                135                140
209 Asn Arg Gly Lys Phe Xaa Val Glu Thr Phe Arg Lys Lys Tyr Asn Leu
210 145              150                155                160
212 Gly Ala Pro Val Ala Gly Thr Cys Tyr Gln Ala Glu Trp Asp Asp Tyr
213            165                170                175
215 Val Pro Lys Leu Tyr Glu Gln Leu Ser Gly Lys
216            180                185
218 <210> SEQ ID NO: 4
```

W--> (line 209)

```
219 <211> LENGTH: 187
220 <212> TYPE: PRT
221 <213> ORGANISM: Drosophila
223 <400> SEQUENCE: 4
225 Met Ser Asp Ser Thr Val Cys Phe Ser Lys His Lys Ile Val Pro Asp
226 1               5                   10                  15
228 Ile Leu Lys Thr Cys Pro Ala Thr Leu Leu Thr Val Thr Tyr Gly Gly
229             20                  25                  30
231 Gly Gln Val Val Asp Val Gly Gly Glu Leu Thr Pro Thr Gln Val Gln
232         35                  40                  45
234 Ser Gln Pro Lys Val Lys Trp Asp Ala Asp Pro Asn Ala Phe Tyr Thr
235     50                  55                  60
237 Leu Leu Leu Thr Asp Pro Asp Ala Pro Ser Arg Lys Glu Pro Lys Phe
238 65                  70                  75                  80
240 Arg Glu Trp His His Trp Leu Val Val Asn Ile Pro Gly Asn Gln Val
241             85                  90                  95
243 Glu Asn Gly Val Val Leu Thr Glu Tyr Val Gly Ala Gly Pro Pro Gln
244             100                 105                 110
246 Gly Thr Gly Leu His Arg Tyr Val Phe Ile Val Phe Lys Gln Pro Gln
247         115                 120                 125
249 Lys Leu Thr Cys Asn Glu Pro Lys Ile Pro Lys Thr Ser Gly Asp Lys
250     130                 135                 140
252 Arg Ala Asn Phe Ser Thr Ser Lys Phe Met Ser Lys Tyr Lys Leu Gly
253 145                 150                 155                 160
255 Asp Pro Ile Ala Gly Asn Phe Phe Gln Ala Gln Trp Asp Asp Tyr Val
256             165                 170                 175
258 Pro Lys Leu Tyr Lys Gln Leu Ser Gly Lys Lys
259             180                 185
261 <210> SEQ ID NO: 5
262 <211> LENGTH: 220
263 <212> TYPE: PRT
264 <213> ORGANISM: C. elegans
266 <400> SEQUENCE: 5
268 Met Val Val Leu Val Thr Arg Ser Leu Leu Pro Ala Leu Phe Phe Ala
269 1               5                   10                  15
271 Ser Arg Ala Pro Phe Ala Ala Ala Thr Thr Ser Ala Arg Phe Gln Arg
272             20                  25                  30
274 Gly Leu Ala Thr Met Ala Ala Glu Ala Phe Thr Lys His Glu Val Ile
275         35                  40                  45
277 Pro Asp Val Leu Ala Ser Asn Pro Pro Ser Lys Val Ser Val Lys
278     50                  55                  60
280 Phe Asn Ser Gly Val Glu Ala Asn Leu Gly Asn Val Leu Thr Pro Thr
281 65                  70                  75                  80
283 Gln Val Lys Asp Thr Pro Glu Val Lys Trp Asp Ala Glu Pro Gly Ala
284             85                  90                  95
286 Leu Tyr Thr Leu Thr Lys Thr Asp Pro Asp Ala Pro Ser Arg Lys Glu
287         100                 105                 110
289 Pro Thr Tyr Arg Glu Trp His His Trp Leu Val Val Asn Ile Pro Gly
290         115                 120                 125
```

```
RAW SEQUENCE LISTING              DATE: 05/14/2001
PATENT APPLICATION:  US/09/654,281   TIME: 12:18:24

Input Set : A:\ES.txt
Output Set: N:\CRF3\05142001\I654281.raw

292 Asn Asp Ile Ala Lys Gly Asp Thr Leu Ser Glu Tyr Ile Gly Ala Gly
293     130             135             140
295 Pro Pro Lys Thr Gly Leu His Arg Tyr Val Tyr Leu Ile Tyr Lys Gln
296 145             150             155             160
298 Ser Gly Arg Ile Glu Asp Ala Glu His Gly Arg Leu Thr Asn Thr Ser
299             165             170             175
301 Gly Asp Lys Arg Gly Gly Trp Lys Ala Ala Asp Phe Val Ala Lys His
302             180             185             190
304 Lys Leu Gly Ala Pro Val Phe Gly Asn Leu Phe Gln Ala Glu Tyr Asp
305         195             200             205
307 Asp Tyr Val Pro Ile Leu Asn Lys Gln Leu Gly Ala
308     210             215             220
310 <210> SEQ ID NO: 6
311 <211> LENGTH: 181
312 <212> TYPE: PRT
313 <213> ORGANISM: Antirrhinum-CEN
315 <400> SEQUENCE: 6
317 Met Ala Ala Lys Val Ser Ser Asp Pro Leu Val Ile Gly Arg Val Ile
318 1           5               10              15
320 Gly Asp Val Val Asp His Phe Thr Ser Thr Val Lys Met Ser Val Ile
321             20              25              30
323 Tyr Asn Ser Asn Asn Ser Ile Lys His Val Tyr Asn Gly His Glu Leu
324         35              40              45
326 Phe Pro Ser Ala Val Thr Ser Thr Pro Arg Val Glu Val His Gly Gly
327     50              55              60
329 Asp Met Arg Ser Phe Phe Thr Leu Ile Met Thr Asp Pro Asp Val Pro
330 65              70              75              80
332 Gly Pro Ser Asp Pro Tyr Leu Arg Glu His Leu His Trp Ile Val Thr
333             85              90              95
335 Asp Ile Pro Gly Thr Thr Asp Ser Ser Phe Gly Lys Glu Val Val Ser
336             100             105             110
338 Tyr Glu Met Pro Arg Pro Asn Ile Gly Ile His Arg Phe Val Phe Leu
339         115             120             125
341 Leu Phe Lys Gln Lys Lys Arg Gly Gln Ala Met Leu Ser Pro Pro Val
342     130             135             140
344 Val Cys Arg Asp Gly Phe Asn Thr Arg Lys Phe Thr Gln Glu Asn Glu
345 145             150             155             160
347 Leu Gly Leu Pro Val Ala Ala Val Phe Phe Asn Cys Gln Arg Glu Thr
348             165             170             175
350 Ala Ala Arg Arg Arg
351             180
353 <210> SEQ ID NO: 7
354 <211> LENGTH: 176
355 <212> TYPE: PRT
356 <213> ORGANISM: Aradopsis-TFL1
358 <400> SEQUENCE: 7
360 Met Glu Asn Met Gly Thr Arg Val Ile Glu Pro Leu Ile Met Gly Arg
361 1           5               10              15
363 Val Val Gly Asp Val Leu Asp Phe Phe Thr Pro Thr Thr Lys Met Asn
```

Please Note:
Use of n and/or Xaa have been detected in the Sequence Listing. Please review the Sequence Listing to ensure that a corresponding explanation is presented in the <220> to <223> fields of each sequence which presents at least one n or Xaa.

VERIFICATION SUMMARY   DATE: 05/14/2001
PATENT APPLICATION: US/09/654,281   TIME: 12:18:25

Input Set : A:\ES.txt
Output Set: N:\CRF3\05142001\I654281.raw

L:25 M:220 C: Keyword misspelled or invalid format, <213> ORGANISM for SEQ ID#:1
L:117 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:1
L:120 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:1
L:123 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:1
L:209 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:3
L:460 M:220 C: Keyword misspelled or invalid format, <213> ORGANISM for SEQ ID#:10
L:474 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:10
L:480 M:220 C: Keyword misspelled or invalid format, <213> ORGANISM for SEQ ID#:11